

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM B

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1: P53909. Adenosine deamina...[gi:1703166] [Related Sequences](#), [PubMed](#), [Taxonomy](#), [BLink](#), [LinkOut](#)

LOCUS ADA_YEAST 347 aa linear PLN 16-OCT-2001

DEFINITION Adenosine deaminase (Adenosine aminohydrolase).

ACCESSION P53909

PID g1703166

VERSION P53909 GI:1703166

DBSOURCE swissprot: locus ADA_YEAST, accession P53909; class: standard.

created: Oct 1, 1996.

sequence updated: Oct 1, 1996.

annotation updated: Oct 16, 2001.

xrefs: gi: gi: [861113](#), gi: gi: [854497](#), gi: gi: [1302088](#), gi: gi: [1302089](#)

xrefs (non-sequence databases): SGD S0005085, InterPro IPR001365, Pfam PF00962, PROSITE PS00485

KEYWORDS Hydrolase; Nucleotide metabolism.

SOURCE baker's yeast.

ORGANISM [Saccharomyces cerevisiae](#)

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (residues 1 to 347)

AUTHORS Mallet,L., Bussereau,F. and Jacquet,M.

TITLE A 43.5 kb segment of yeast chromosome XIV, which contains MFA2, MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an adenosine deaminase gene and 14 new open reading frames

JOURNAL Yeast 11 (12), 1195-1209 (1995)

MEDLINE [96109932](#)

REMARK SEQUENCE FROM N.A.

STRAIN=S288C

COMMENT -----

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[CATALYTIC ACTIVITY] ADENOSINE + H(2)O = INOSINE + NH(3) (ALSO ACTS ON DEOXYADENOSINE).

[SIMILARITY] BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.

FEATURES Location/Qualifiers

source 1..347
 /organism="Saccharomyces cerevisiae"
 /db_xref="taxon:4932"

Protein 1..347
 /product="Adenosine deaminase"
 /EC_number="3.5.4.4"

Site 204
 /site_type="active"
 /note="POTENTIAL."

Site 252
/site_type="active"
/note="POTENTIAL."
Site 285
/site_type="active"
/note="POTENTIAL."
Site 286
/site_type="active"
/note="POTENTIAL."
ORIGIN
1 mvsveflqel pkcehhlhle gtlepdllfp laskrndiilp egfpksveel nekykkfrdl
61 qdfldyyig tnvlideqdf fdawayfkk vhkqglvhae vfydpqshts rgisietvtk
121 gfqracdkaf sefgitskli mcllrhiepe eclktieeat pfikdgtsa lgldsaekpf
181 pphlfvecyg kaaslnkdlk latahageegp aqfvsdaldl lqvtridhgi nsqydeelld
241 rlsrdqtmjt icplsnvkq vvqsvselpi qkf1drdvpf slnsddpayf ggyildvytq
301 vskdfphwdh etwgriakna ikgswcddkr knqlsrvde vvtkysh
//

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1: AAA62126. AMP deaminase iso...
[gi:644509]

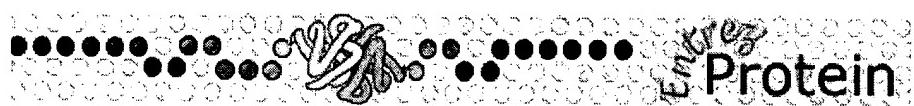
Nucleotide, Related Sequences, Taxonomy, BLink,
LinkOut

LOCUS AAA62126 753 aa linear PRI 08-FEB-1995
 DEFINITION AMP deaminase isoform L splicing variant.
 ACCESSION AAA62126
 PID g644509
 VERSION AAA62126.1 GI:644509
 DBSOURCE locus HUMAMPD2 accession M91029.1
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 753)
 AUTHORS Van den Bergh, F. and Sabina, R.L.
 TITLE Exon shuffling at the 5' end of the human AMPD2 gene produces
 multiple transcripts encoding variable N-terminal extensions of
 isoform L
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 753)
 AUTHORS Sabina, R.L.
 TITLE Direct Submission
 JOURNAL Submitted (06-OCT-1994) Richard L Sabina, Biochemistry, Medical
 College of Wisconsin, 8701, Watertown Plank Road, Milwaukee,
 Wisconsin, 53226, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..753
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="T-lymphoblast"
 /tissue_type="placenta fetal heart"
 Protein 1..753
 /product="AMP deaminase isoform L splicing variant"
 /EC_number="3.5.4.6"
 CDS 1..753
 /gene="AMPD2"
 /coded_by="join(M91029.1:<1..7,M91029.1:236..2491)"
 ORIGIN
 1 aeelftrs1a eselrsapye fpeespieql eerrqrlerq isqdvklepd illrakqdf1
 61 ktdsdslql ykeqgeggd rslrerdlve refqrvtisg eekcgvpftd lldaaksvvrr
 121 alfirekyma lslqsfcppt rrylqlaek pletrtyeqg pdtpvsadap vhppaleqhp
 181 yehcepstmp gd1glglrmv rgvvhvyytr epdehcseve lpypdqlqefv advnvlmali
 241 ingpiksfcy rrlqylsskf qmhvllnemk elaaqkkvph rdfynirkvd thihasscmn
 301 qkhllrfikr amkrhleeiv hveggreqtl revfesmnlt aydlsvdtld vhadrntfhr
 361 fdkfnakynp igesvlreif iktdnrvgsk yfahiikevm sdleeskyqn aelrlsiygr
 421 srdewdklar wavmhrvhsp nvrwlqvpr lfdvyrtkgq lanfqemlen iflplfeatv
 481 hpashpelhl flehvdgfd s vddeskpenh vfnlesplpe awveednppy aaylyytfan
 541 mamlnhlrrq rgfhtfvlp hcgeagpihh lvsafmlaen ishgllirka pvlqylyyla
 601 gigiamspls nnslflyhr nplpeylsrg lmvslstddp lqfhftkepl meeysiatqv

661 wklsscdmce larnsvlmsg fshkvkshwl gpnytkegpe gndirrtnvp dirvgyryet
721 lcqelalitq avqsemleti peeagitmsp gpq
//

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Display <input type="button" value="default"/>		<input type="button" value="Save"/>	<input type="button" value="Text"/>	<input type="button" value="Add to Clipboard"/>		Preview/Index	History	Clipboard
						Limits		Details

1: AAD03459. contains similarity...[gi:4115949] Nucleotide, Related Sequences, Taxonomy, BLINK, LinkOut

LOCUS AAD03459 275 aa linear PLN 10-AUG-1999
 DEFINITION contains similarity to adenosine deaminases [Arabidopsis thaliana].
 ACCESSION AAD03459
 PID g4115949
 VERSION AAD03459.1 GI:4115949
 DBSOURCE locus T4B21 accession AF118223.2
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (residues 1 to 275)
 REFERENCE AUTHORS Abbott,A., Kock,J. and Lehnert,L.
 TITLE The sequence of *A. thaliana* T4B21
 JOURNAL Unpublished
 REFERENCE AUTHORS Washington University Genome Sequencing Center.
 TITLE The *A. thaliana* Genome Sequencing Project
 JOURNAL Unpublished
 REFERENCE AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JAN-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (06-AUG-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT Method: conceptual translation.
 FEATURES source Location/Qualifiers
 Protein 1..275
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="IV"
 /map="unknown"
 /clone="T4B21"
 CDS 1..275
 /name="contains similarity to adenosine deaminases"
 1..275
 /gene="T4B21.20"
 /coded_by="complement(join(AF118223.2:80842..80913,

AF118223.2:80994..81107,AF118223.2:81196..81265,
AF118223.2:81344..81720,AF118223.2:81791..81850,
AF118223.2:82153..82210,AF118223.2:82365..82441))"

ORIGIN

1 mewiqslpki elhahlngsi rdstllelar vlgekgvivf advehvvvedf alenvvylel
61 rttppkrssdi gmskrssymeal viqglrvse vdidfvtaasd sqklhnagdg igrkkiyvrl
121 llsidrrett esametvs vs kqakllrilk rlmqktfdtl lfslkvklal emrdvgvvgi
181 dlsgnplvge wstflpalqy akdndlhitl hcgevpnpke iqaml dfkph righacffkd
241 edwtklksfr ipveicltsn ivtksissid ihhfg

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1: 1002274A[gi:351916]

LOCUS 351916 105 aa linear VRT 20-JUN-1996
DEFINITION cytochrome c.
ACCESSION 351916
PID g351916
VERSION GI:351916
DBSOURCE prf: locus 1002274A;
state: myeloma/lymphoma;
taxonomy: Aves.
KEYWORDS Cytochrome c Gene Allele; Chicken; Genomic Blot Hybridization; Seq Determination; 104AAs; 1600bp; Limited Polymorphism; 1 Enz in Chicken Genome.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (residues 1 to 105)
AUTHORS Limbach, K.J. and Wu, R.
TITLE Isolation and characterization of two alleles of the chicken cytochrome c gene
JOURNAL Nucleic Acids Res. 11 (24), 8931-8950 (1983)
MEDLINE 84169527
COMMENT gene CC9/CC10.
FEATURES Location/Qualifiers
source 1..105
/organism="Gallus gallus"
/db_xref="taxon:9031"
ORIGIN
1 mgdiekgkki fvqkcsqcht veckggkhktg pnlhglfgrk tgqaegfsyt danknkgitw
61 gedtlmeyle npkkyipgtk mifagikkks ervdliaylk datsk
//

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1: P22333. ADENOSINE DEAMINA...
[gi:2506342]

[Related Sequences](#), [PubMed](#), [Taxonomy](#), [BLink](#),
[LinkOut](#)

LOCUS ADD_ECOLI 333 aa linear BCT 20-AUG-2001
 DEFINITION ADENOSINE DEAMINASE (ADENOSINE AMINOHYDROLASE).
 ACCESSION P22333
 PID g2506342
 VERSION P22333 GI:2506342
 DBSOURCE swissprot: locus ADD_ECOLI, accession P22333;
 class: standard.
 extra accessions:P78240,P78163,created: Aug 1, 1991.
 sequence updated: Nov 1, 1997.
 annotation updated: Aug 20, 2001.
 xrefs: gi: gi: 145200, gi: gi: 145201, gi: gi: 2367121, gi: gi:
1787910, gi: gi: 1742665, gi: gi: 1742677, gi: gi: 1742679, gi: gi:
1742685, gi: gi: 1742692, gi: gi: 1742693, gi: gi: 1742711, gi: gi:
1742717, gi: gi: 95641
 xrefs (non-sequence databases): HSSP P03958, EcoGene EG10030,
 InterPro IPR001365, Pfam PF00962, PROSITE PS00485
 KEYWORDS Hydrolase; Nucleotide metabolism; Complete proteome.
 SOURCE Escherichia coli.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.
 REFERENCE 1 (residues 1 to 333)
 AUTHORS Chang,Z.Y., Nygaard,P., Chinault,A.C. and Kellems,R.E.
 TITLE Deduced amino acid sequence of Escherichia coli adenosine deaminase
 reveals evolutionarily conserved amino acid residues: implications
 for catalytic function
 JOURNAL Biochemistry 30 (8), 2273-2280 (1991)
 MEDLINE 91152042
 REMARK SEQUENCE FROM N.A.
 STRAIN=K12
 REFERENCE 2 (residues 1 to 333)
 AUTHORS Blattner,F.R., Plunkett,G.I.I.I., Bloch,C.A., Perna,N.T.,
 Burland,V., Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K.,
 Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A.,
 Rose,D.J., Mau,B. and Shao,Y.
 TITLE The complete genome sequence of Escherichia coli K-12
 JOURNAL Science 277 (5331), 1453-1474 (1997)
 MEDLINE 97426617
 REMARK SEQUENCE FROM N.A.
 STRAIN=K12 / MG1655
 REFERENCE 3 (residues 1 to 333)
 AUTHORS Aiba,H., Baba,T., Fujita,K., Hayashi,K., Inada,T., Isono,K.,
 Itoh,T., Kasai,H., Kashimoto,K., Kimura,S., Kitakawa,M.,
 Kitagawa,M., Makino,K., Miki,T., Mizobuchi,K., Mori,H., Mori,T.,
 Motomura,K., Nakade,S., Nakamura,Y., Nashimoto,H., Nishio,Y.,
 Oshima,T., Saito,N., Sampei,G., Seki,Y., Sivasundaram,S.,
 Tagami,H., Takeda,J., Takemoto,K., Takeuchi,Y., Wada,C.,
 Yamamoto,Y. and Horiuchi,T.

TITLE A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map

JOURNAL DNA Res. 3 (6), 363-377 (1996)

MEDLINE 97251357

REMARK SEQUENCE FROM N.A.

STRAIN=K12

COMMENT On Oct 9, 1997 this sequence version replaced gi:113347.

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[CATALYTIC ACTIVITY] ADENOSINE + H(2)O = INOSINE + NH(3) (ALSO ACTS ON DEOXYADENOSINE).

[SIMILARITY] BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.

FEATURES

source	Location/Qualifiers 1..333 /organism="Escherichia coli" /db_xref="taxon:562"
Protein	1..333 1..333 /product="ADENOSINE DEAMINASE"
Region	/EC_number="3.5.4.4" 145 /region_name="Conflict"
Site	/note="MISSING (IN REF. 1)." 197 /site_type="active"
Site	/note="POTENTIAL." 245 /site_type="active"
Site	/note="POTENTIAL." 278 /site_type="active"
Site	/note="POTENTIAL." 279 /site_type="active"

ORIGIN

1 midttlpltd ihrhldgnir pqtilelgrq ynislpaqsl etliphvqvi anepdlvsfl
61 tkldwgkvkl asldacrrva feniedaarh glhyvelrfs pgymamahql pvagvveavi
121 dvgregcrtf gvqakligim srtfgeaacq geleafahr dqitalddag delgfpgsif
181 lshfnrarda gwhitvhage aagpesiwqa irelgaerig hgvkaiedra lmdflaeqqi
241 giescltsni qtstvaelaa hplktflehg irasintddp gvqgvdiihe ytvaapaagl
301 sreqirqaqi nglemaflsa eekralrekv aak

//

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